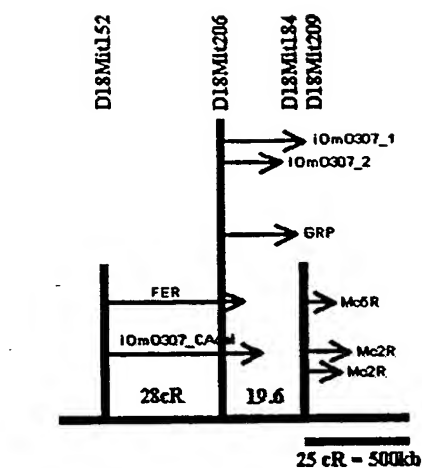


FIG. 1



FER	31.01 cR from D18Mit152 (lod >3.0)
10m0307_CA	30.10 cR from D18Mit152 (lod >3.0)
10m0307_2	12.00 cR from D18Mit206 (lod >3.0)
GRP	16.40 cR from D18Mit206 (lod >3.0)
10m0307_1	18.87 cR from D18Mit206 (lod >3.0)
Mc5R	7.04 cR from D18Mit209 (lod >3.0)
Mc2R ACTHR_1	10.09 cR from D18Mit209 (lod >3.0)
Mc2R ACTHR_2	7.30 cR from D18Mit209 (lod >3.0)

*CA repeat removed from the sequence against which probes were generated

52.4 cR/M, ~20kb/cR

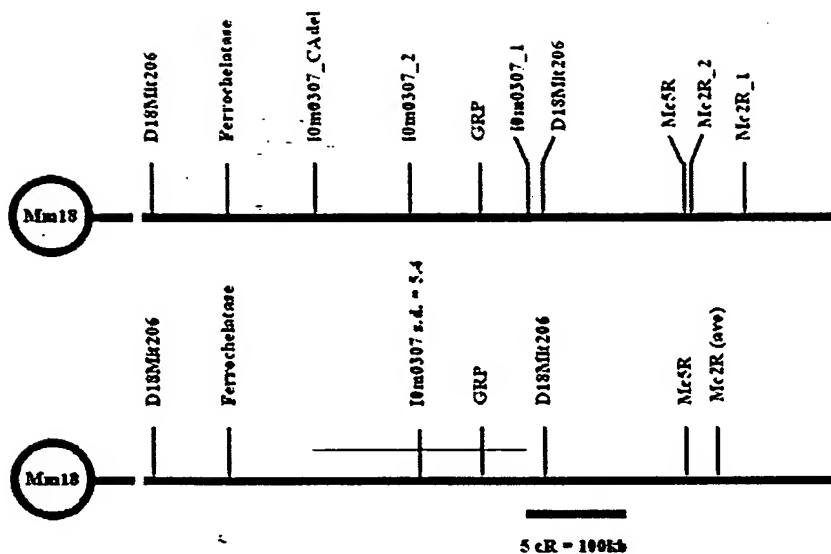


FIG. 2

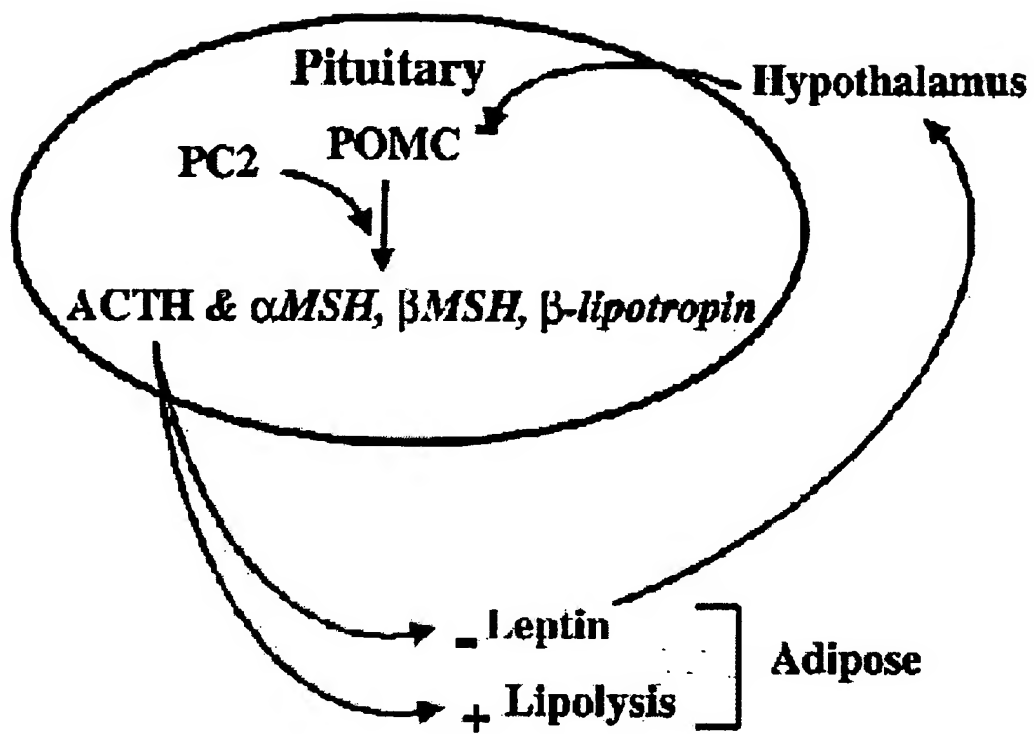


FIG. 3

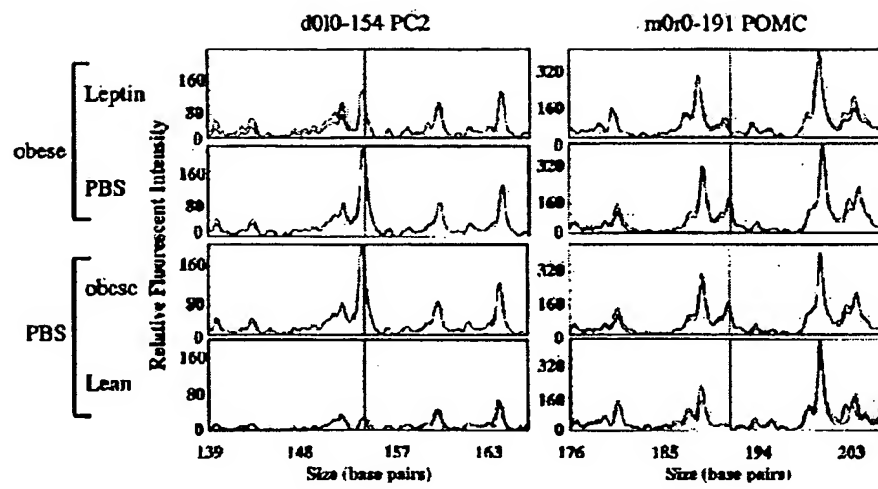
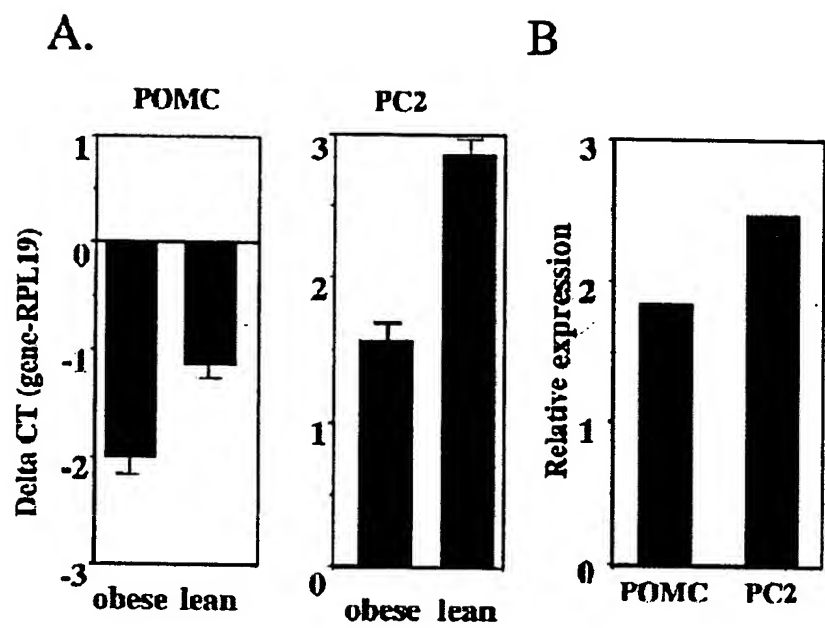


FIG. 4



Six-Frame Translation Analysis of 1.02b_i0m0307FLS_REVCOMP

(Linear) MAP of: /opt/curagen/curatools/sessions/dlewin/projects/default/S/1.02b_i0m0307FLS_REVCOMP/gcg_orf_map/409:

1.02b_i0m0307FLS_REVCOMP

1 AAGGAGGGCCAGTCGCAAAACATTATTATTCAGTATATTGCTTACAAAAGTTACACAGTA + 60
TTCCCTCCCGGGTCAGCGTTTTGTAATAACGTCATATAACGAATGTTTCAATGTGTCAT

a K G G P S R K T F I A V Y C L Q S Y T V -
b R E G P V A K H L Q Y I A Y K V T Q Y -
c G R A Q S Q N I Y C S I L L T K L H S I -
1 -----+ 60
d P L A W D C F M * Q L I N S V F N C L -
e L S P G T A F C K N C Y I A * L T V C Y -
f P P G L R L V N I A T Y Q K C L * V T -

61 TATTATAATCAATTCAGTGGATTATTTACTATTAGTAGTTGTTTATTCTTCCTTTGC + 120
ATAATATTAGTAAGATTACACTCAATAAATGATAATCATCAACAAATAAAGAAACG

a Y Y N H S N V S Y L L L V V V Y F L C -
b I I I I L M * V I Y Y * * L F I S S F A -
c L * S F * C E L F T I S S C L F L P L P -
61 -----+ 120
d I N Y D N * H S N N V I L L Q K N R G K -
e I I I M R I H T I * * * Y N N I E E K A -
f Y * L * E L T L * K S N T T * K K R Q -

121 CTAATTACAAGTTACACTTTATCATAAGCATAAATGAATACAGAAAAACAGCACACA + 180
GATTAAATGTTCAATGGAATAGTATTCGTATTACTTACTTATGCTTTTGTCTGTGT

a L I Y K L H F I I S I N E Y R K T G H T -
b * F T S Y T L S * A * M N T E K Q D T Q -
c N L Q V T L Y H K H K * I Q K N R T H R -
121 -----+ 180
d G L K C T V S * * L C L H I C F F L V C -
e * N V L * V K D Y A Y I F V S F C S V C -

R I * L N C K I M L M F S Y L F V P C V -
 GGGCTGATAGTCTGCAGCTTCCACCATCCATCCATGGGGGACTCCTGAGATGTACCCGG 240
 CCCCAGCTATCAGACGTCGAAGTGGTAGGTAGGTACCCCTGAGGACTCTACATGGGCC
 181

a	G	A	D	S	L	Q	L	P	P	S	I	H	G	G	L	L	R	C	T	R	-
b	G	L	I	V	C	S	F	H	H	P	S	M	G	D	S	*	D	V	P	G	-
c	G	*	S	A	A	S	T	I	H	P	W	G	T	P	E	M	Y	P	V	-	
	181	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	240	
d	L	P	Q	Y	D	A	A	E	V	M	W	G	H	P	V	G	S	I	Y	G	-
e	P	P	S	I	T	Q	L	K	W	G	D	M	P	S	E	Q	S	T	G	P	-
f	P	A	S	L	R	C	S	G	G	D	M	W	P	P	S	R	L	H	V	R	-

241 TGTAGAGTAAAGAGGAGCGCTCTAGCTTCTTAGGGATGCTCTAACAAAAATACTACAACATAA 300
ACATCTCAATTCTCTCGGAGATCGAAGGATCCCTACGAGATTGTTTATGATGTTGATT

a	C R V R G A L * L P R D A L T K Y Y N *	-
b	V E * E R R S S F L G M L * Q N T T K	-
c	* S K R S A L A S * G C S N K I L Q L S	-
	241-----+-----+-----+ 300	
d	T Y L L L A R A E * P H E L L I S C S	-
e	T S Y S S R E L K R P I S * C F V V V L	-
f	H L T L P A S * S G L S A R V F Y * L *	-

GTGGCTCAAAAACAACAGAAATGTCGTCTGTCTCACTGTCTGGCAGCCAGATGTCGTGT
-----+-----+-----+-----+-----+-----+ 360
CACCGAGTTTGTGCTTTACAGACAGACAGAGTGTGACGACCGTCGGTCTACAGCACA

a	V A Q N N R N V C L S H T A G S Q M S C -
b	W L K T T E M S V C L T L L A A R C R V -
c	G S K Q Q K C L S V S H C W Q P D V V C -
	301-----+-----+-----+ 360
d	L P E F C C F H R D T E C Q Q C G S T T -
e	H S L V V S I D T Q R V S S A A L H R T -
f	T A * F L L F T Q R D * V A P L W I D H -

361 GTGTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCTTCTCTAGAGC
-----+-----+-----+-----+
CACACACACACACACACACACACACACACATCTAGAAGAGATCTCG

a	V C V C V C V C V C V C V C V C V D L * S -
b	C V C V C V C V C V C V C V C V * I F S R A -
c	V C V C V C V C V C V C V C V C R S S L E L - -----+-----+-----+-----+-----+ 420 361 H T H T H T H T H T H T H T H T H L D E R S -
d	H T H T H T H T H T H T H T Y I K E L A -
e	H T H T H T H T H T H T H T Y I K E L A -

T H T H T H T H T H T H T H T S R R * L -

421 TCTAAATAGGCTTCTCACAGCTTCCCGAAGTGTGGTCTCTCTGAGATGGAAGATGG + 480
AGATTATCCGAAGAGTGTGGAAGGGCTTCACAAACCAGGAAGGACTCTACCTTCTACC

a S K I G F S Q L P E V F G P S * D G R W -
b L K * A S H S F P P K C L V L P E M E D G -
c * N R L L T A S R S V W S F L R W K M V - 480
421 S * F L S R V A E R L T Q D K R L H F I -
d R F Y A E * L K G F H K T R G S I S S P -
e E L I P K E C S G S T N P G E Q S P L H -
f

TTGGTCATCTTCATTGCTGCTGCTTCATCGCCCTCTGTGTGTCTCTTTTACA + 540
481 AACCAAGTAGAAGTACAGACAGCTAAAGTAGCGGGGAGACACACAGAGAAAAATGT

a L V I F I Q C L H F I A P L C V S L F T -
b W S S S F S V C I S S P L C V C L F L Q -
c G H L H S V S A F H R P P S V C V S F Y K - 540
481 T P * R * E T D A N * R G E T H T E K * -
d Q D D E N L T Q M E D G R Q T H R K K C -
e N T M K M * H R C K M A G R H T D R K V -
f

AGGACACTGTGGTTCATTACCTGGGGCTCTTACCTCAGTGACCTCAATGACCCCTGGA + 600
541 TCCTGTGACACCCAGTAAGTGGACCCCGGAGGAATGGAGTCAGTGAGTTACTGGGACCT

a R T L W V I H L G P P Y L S D L N D P G -
b G H C G S F T W G L L T S V T S M T L E -
c D T V G H S P G A S L P Q * P Q * P W K - 600
541 L S V T P * E G P A E K G * H G * H G Q -
d P C Q P D N V Q P R R V E T V E I V R S -
e L V S H T M * R P G G * R L S R L S G P -
f

AATCATTCTCTAAAAGACAAACACTTGGAGGTACGGGGACTACTATAGCATGTTATAG + 660
601 TTAGTAAGAGAGATTTTCTGTGTGAACCTCCATGCCCTGATGATATCGTACAATATC

a N H S L * K D N T W R Y G D Y Y S M L * -
b I I L S K K T T L G G T G T T I A C Y R -
c S F S L K R Q H L E V R G L L * H V I E - 660
601 F D N E R F L C C K S T R P S S Y C T I -
d I M R E L F V V S P P V P V I A H * L -
e

f F * E R * F S L V Q L Y P S * * L M N Y -
AAAGCTATGTCACGTGACTTTCGTGAGAAATAACAGCGTTATATAACCTCATGAGCTTCAAG 720
661 TTTTCGATACAGTGCAGCTGAAAGCACTCTTATTGTTCGCAATATTGGAGTACTCGAAGTTC

a K A M S R D F R E N N S V I N L M S F K -
b K L C H V T F V R I T A L * T S * A S R -
c S Y V T * L S * E * Q R Y K P H E L Q D -
661 S L * T V H S E H S Y C R * L G * S S * -
d F S H * T V K T L I V A N Y V E H A E L -
e F A I D R S K R S F L L T I F R M L K L -
f

ACTTAGATTATGATACCTGTACTACATTAGGTAACCTGCTTAACGTTAAAGTGTACAGCTGA 780
721 TGAATCTAATACTATGGACATGATGTAATCCATTGACGAATTGCAATTTTCACAGTCGACT

a T * I M I P V L H * V T A * R * S V S * -
b L R L * Y L Y Y I R * L L N V K V S A E -
c L D Y D T C T T L G N C L T L K C Q L R -
721 S K S * S V Q V V N P L Q K V N F H * S -
d S L N H Y R Y * M L Y S S L T L T D A S -
e V * I I I G T S C * T V A * R * L T L Q -
f

GGCACCTTAAAGGGTTACAGTGTATCTGAGCAAAACACCAGTTGTTGCTGGGCAGCTCCAA 840
781 CCGTGAATTTCCCAATGTCACATAGACTCGTTTGTGGTCAACAACGACCCGTCGAGGTT

a G T L K G Y S V S E Q T P V V A G Q L Q -
b A P * R V T V Y L S K H Q L L L G S S N -
c H L K G L Q C I * A N T S C C W A A P T -
781 L C R L P N C H I Q A F V L Q Q A A G -
d A G * L T V T Y R L L C W N N S P L E L -
e P V K F P * L T D S C V G T T A P C S W -
f

CCCTGTGTGCCCCAGGCACCTTCAGGTGGGAACTAACTATTAGGGAGGCATAAACGCCA 900
841 GGGACACACCGGGTCCGTGAAGTCCACCCCTTGATTGAGTAATCCCTCCGTATTGCGGT

a P L C G P G T S G G N * L I R E A * T P -
b P C V A Q A L Q V G T N S L G R H K R Q -
c P V W P R H F R W E L T H * G G I N A K -
841 V G T H G L C K L H S S V * * P P M F A -
d G Q T A W A S * T P V L E N P L C L R W -
e

f G R H P G P V E P P F * S M L S A Y V G -

901 AGCCAACGTTGATTGGTTACAGCTCCACAGCTGTTTATTGTCCTCTTCCCATTTGGAGAGT
TCGGTTGCACTAACCAATGTCGAGGTGTCGACAAATAAACCGGAGAAGGGTAACCTCTCA

a S Q R D W L Q L H S C L F G L F P L E S -
b A N V I G Y S S T A V Y L A S S H W R V -
c P T * L V T A P Q L F I W P L P I G E S -
901 L G V H N T V A G C S N I Q G R G M P S -
d A L T I P * L E V A T * K A E E W Q L T -
e L W R S Q N C S W L Q K N P R K G N S L -
f

961 CCCTAGTTATATAAAATTTGGCTGCCATGGATTGGTTGAGTTTGGTTTCTTTTA
GGGATCAATATATATTTTAAACCGGCTACCTAACCAACTCAAAACAAAACCAAAAGAAAT

a P * L Y K I L A A M D W L S L F W F S L -
b P S Y I K F W L P W I G * V C F G F L * -
c L V I * N F G C H G L V E F V L V F F N -
961 D R T I Y F K P Q W P N T S N T K T K K -
d G L * I F N Q S G H I P Q T ' Q K P K R * -
e G * N Y L I K A A M S Q N L K N Q N E K -
f

1021 ATATACAAATCTATTTAAAGTAGTTTATATACATATAATAATAATAATAATCTTTTTA
TATATGTTTAGATAAAATTTTCATCAATAATAGTGTATATTTATTTATTAGAAAAAAT

a I Y K S I * S S L Y H I * * I N K S F L -
b Y T N L F K V V Y I T Y N K * I N L F * -
c I Q I Y L K * F I S H I I N K * I F F K -
1021 L I C I * K F Y N I D C I I F L Y I K K -
d Y V F R N L T T * I V Y L L Y I F R K * -
e I Y L D I * L L K Y * M Y Y I F L D K K -
f

1081 AAAAACTTTTGTTCATAATCATGAAAGCTAAGTCACGTAGGAGAAGACCATGA
TTTTTTGAAAAACAAAGTTTAGTCGTTTCGATTCCAGTCATCCTCTTCTGGTACT

a K K L F C F Q I M Q S * G H V G E R P * -
b K N F F V F K S C K A K V T * E K D H D -
c K T F L F S N H A K L R S R R K T M T -
1081 L F V K K N E F * A F S L D R L L F V M -
d F F K K K T K L D H L A L T V Y S F S W S -
e

```

f      F F S K Q K * I M C L * P * T P S L G H -
1141  CTGTGCGCCTTTTATGCTTTGGGTCTGGTCTCCATTTTAATACACTATGGTCA
      GACACACGGAAAAATACGAAACCCAGACAGAGGTAAAAATATGAAATGTGATACCAGT
      1200

a      L C A F L C F G S G L H F N T L T L W S -
b      C V P F Y A L G L V S I L I L * H Y G Q -
c      V C L F M L W V W S P F * Y F N T M V S -
1141  V T H R K I S Q T Q D G N * Y K L V I T -
      Q T G K * A K P R T E M K I S * C * P * -
f      S H A K K K H K P D P R W K L V K V S H D -

      GTTACTGATACAGAAAAATCAAAATCCAAGCCCAAGATAA (SEQIDNO: 20)
1201  -----
      CAATGACTATGCTCTTTTAGTTAGTTAGGTTCTCTATT (SEQIDNO: 21)
      1237

a      V T D T E N Q I Q A K I - (SEQIDNO: 22)
b      L L I Q K I K S K P R * - (SEQIDNO: 23)
c      Y * Y R K S N P S Q D - (SEQIDNO: 24)
1201  -----
d      L * Q Y L F D F G L W S L - (SEQIDNO: 25)
e      N S I C F I L D L G L Y - (SEQIDNO: 26)
f      T V S V S F * I W A L I - (SEQIDNO: 27)

```

Import all sequences checked below:

Note: Stops (*) and ambiguous amino acids (?) are replaced with an X in the importable sequence

- ☐ Frame A (frame 1) translation: KGGPS.....IQAKI
- ☐ Frame B (frame 2) translation: REGPV.....SKPRX
- ☐ Frame C (frame 3) translation: GRAQS.....NPSQD
- ☐ Frame D (frame 4) translation: LSWLG.....DWALP
- ☐ Frame E (frame 5) translation: YLGLD.....TGPSL
- ☐ Frame F (frame 6) translation: ILAWI.....RLGPP